

5' AAA CCT TCA CCT CTC ATG CTG AAG CTC ACA CCC TTG CCC TCC AAG ATG AAG GTT	9	18	27	36	45	54
M L K L T P L P S K M K V						
63 TCT GCA GCG CTT CTG TGC CTG CTG CTG CTG ATG GCA GCC ACT TTC AGC CCT CAG GGA	72	81	90	99	108	
S A A L L C L L L L M A A T F S P Q G						
117 CTT GCT CAG CCA GAT TCA GTT TCC ATT CCA ATC ACC TGC TGC TTT AAC GTG ATC	126	135	144	153	162	
L A Q P D S V S I P I T C C F N V I						
171 AAT AGG AAA ATT CCT ATC CAG AGG CTG GAG AGC TAC ACA AGA ATC ACC AAC ATC	180	189	198	207	216	
N R K I P I Q R L E S Y T R I T N I						
225 CAA TGT CCC AAG GAA GCT GTG ATC TTC AAG ACC AAA CGG GGC AAG GAG GTC TGT	234	243	252	261	270	
Q C P K E A V I F K T K R G K E V C						
279 GCT GAC CCC AAG GAG AGA TGG GTC AGG GAT TCC ATG AAG CAT CTG GAC CAA ATA	288	297	306	315	324	
A D P K E R W V R D S M K H L D Q I						
333 TTT CAA AAT CTG AAG CCA TGA GCC TTC ATA CAT GGA CTG AGA GCT TGA	342	351	360	369	378	
F Q N L K P						

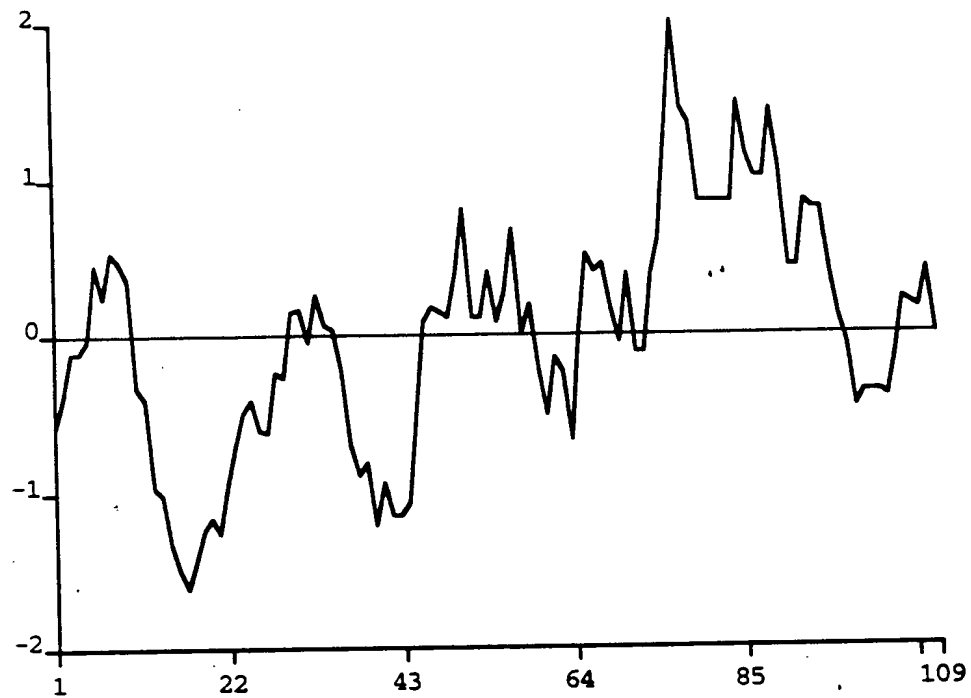
FIGURE 1A

387 396 405 414 423 432  
AGA AAA GCT TAT TTA TTT TCC CCA ACC TCC CCC AGG TGC AGT GTG ACA TTA TTT  
441 450 459 468 477 486  
TAT TAT AAC ATC CAC AAA GAG ATT ATT TTT AAA TAA TTT AAA GCA TAA TAT TTC  
495 504 513 522 531 540  
TTA AAA AGT ATT TAA TTA TAT TTA AGT TGT TGA TGT TTT AAC TCT ATC TGT CAT  
549 558 567 576 585 594  
ACA TCC TAG TGA ATG TAA AAT GCA AAA TCC TGG TGA TGT GTT TTT TGT TTT TGT  
603 612 621 630 639 648  
TTT CCT GTG AGC TCA ACT AAG TTC ACG GCC AAA NGT CAT TGT TCT CCC TCC TAC  
657 666 675 684 693 702  
CNG TNC GTA GTG TTG TGG GGT CCT CCC NTG GAT CAT CAA GGT GAA ACA CTT AGG  
711 720 729 738 747 756  
TAT TCT TTG GCA ATC AGT GCT CCT GTA AGT CAA ATG TGT GCT TTG TAC TGC TGT  
765 774 783 792 801 810  
TGT TGA AAT TGA NGT TAC TGT ANA TAA CTA TGG AAT TTT GAA AAA AAA TTT CAA  
819 828 837 846 855  
AAA GAA AAA NAT ATA TAT AAT TTA AAA CTA AAA AAA AAA AAA A 3'

FIGURE 1B

1	M	L	K	L	T	P	L	P	S	K	M	K	V	S	A	A	L	L	C	L	L	L	M	A	A	T	F	S	P	Q	G	L	A	Q	P	D	S	V	S	I	965517
1	M	W	K	P	M	P	S	P	S	N	M	K	A	S	A	L	L	C	L	L	L	T	A	A	A	F	S	P	Q	G	L	A	Q	P	V	G	I	N	T	GI 288397	
1	M	-	-	-	-	-	-	-	-	-	-	K	V	S	A	A	L	L	C	L	L	I	A	A	T	F	I	P	Q	G	L	A	Q	P	D	A	I	N	A	GI 338809	
41	P	I	T	C	C	F	N	V	I	N	R	K	I	P	I	Q	R	L	E	S	Y	T	R	I	T	N	I	Q	C	P	K	E	A	V	I	F	K	T	K	R	965517
41	S	T	T	C	C	Y	R	F	I	N	K	I	P	K	Q	R	L	E	S	Y	R	R	T	T	S	S	H	C	P	R	E	A	V	I	F	K	T	K	L	GI 288397	
31	P	V	T	C	C	Y	N	F	T	N	R	K	I	S	V	Q	R	L	A	S	Y	R	R	I	T	S	S	K	C	P	K	E	A	V	I	F	K	T	I	V	GI 338809
81	G	K	E	V	C	A	D	P	K	E	R	W	V	R	D	S	M	K	H	L	D	Q	I	F	Q	N	L	K	P												
81	D	K	E	I	C	A	D	P	T	Q	K	W	V	Q	D	F	M	K	H	L	D	K	K	T	Q	T	P	K	L												
71	A	K	E	I	C	A	D	P	K	Q	K	W	V	Q	D	S	M	D	H	L	D	K	Q	T	Q	T	P	K	T												

FIGURE 2



**FIGURE 3**

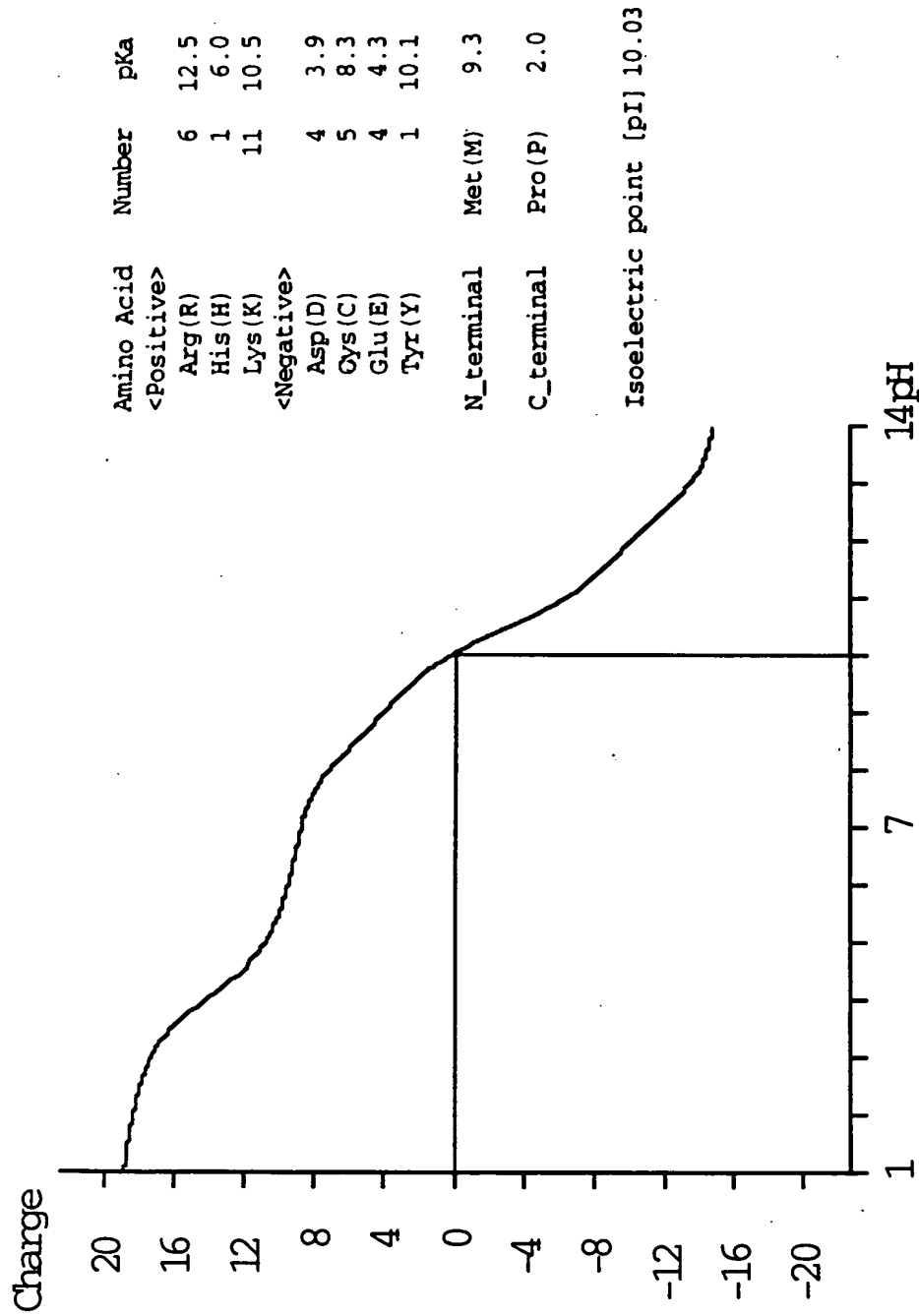


FIGURE 4

The Electronic Northern for clone: 965517  
and Stringency = 50

Library	Lib Description	Abun	Pct	Abun
<u>PANCDIT03</u>	pancrease, NIDDM, 57 M	1	0.145	
<u>MMLR1DT01</u>	macrophages (adher PBMNC), M/F, 24-hr MLR	4	0.094	
<u>MMLR3DT01</u>	macrophages (adher PBMNC), M/F, 72-hr MLR	2	0.066	
<u>MPGHLPT02</u>	macrophages (adher PBMNC), M/F, treated LPS	1	0.049	
<u>TMLR3DT01</u>	lymphocytes (non-adher PBMNC), M, 96-hr MLR	2	0.045	
<u>BLADTUT02</u>	bladder tumor, carcinoma, 80 F	1	0.030	
<u>SYNORAT05</u>	synovium, knee, rheumatiod, 62 F	1	0.028	
<u>LUNGNOM01</u>	lung, 72 M, WM	1	0.026	
<u>MPGHNOT03</u>	macrophages (adher PBMNC), M/F	2	0.025	
<u>BRSTNOT05</u>	breast, 58 F, match to BRSTTUT03	1	0.015	

FIGURE 5